



RAW SEQUENCE LISTING

DATE: 04/23/2002

PATENT APPLICATION: US/09/306,780

TIME: 11:00:00

Input Set : N:\Crf3\RULE60\09306780.raw

Output Set: N:\CRF3\04232002\I306780.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: TAKEMURA, FUMINORI

6 UENO, EIICHI

7 ITOH, SATORU

9 (ii) TITLE OF INVENTION: NUCLEIC ACID-BOUND POLYPEPTIDE, METHOD
 10 OF PRODUCING NUCLEIC ACID-BOUND POLYPEPTIDE AND
 11 IMMUNOASSAY USING THE POLYPEPTIDE.

13 (iii) NUMBER OF SEQUENCES: 20

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 17 P.C.

18 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

19 (C) CITY: ARLINGTON

20 (D) STATE: VA

21 (E) COUNTRY: U.S.A.

22 (F) ZIP: 22202

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/306,780

C--> 32 (B) FILING DATE: 07-May-1999

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/841,657A

38 (B) FILING DATE: 30-APR-1997

40 (A) APPLICATION NUMBER: JP 8-134444

41 (B) FILING DATE: 01-MAY-1997

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: OBLON, NORMAN F.

45 (B) REGISTRATION NUMBER: 24,618

46 (C) REFERENCE/DOCKET NUMBER: 2084-033-0

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (703) 413-3000

50 (B) TELEFAX: (703) 413-2220

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 102 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: single

ENTERED

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59      (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: other nucleic acid
62      (A) DESCRIPTION: /desc = "synthetic DNA"
65      (ix) FEATURE:
66      (A) NAME/KEY: CDS
67      (B) LOCATION: 1..102
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 AGA CGA CGA GGG AGG TCC CCT AGA AGA AGA ACT CCC TCG CCT CGC AGA      48
73 Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg
74 1      5      10      15
76 CGA AGG TCT AAA TCG CCG CGT CGC AGA AGA TCT CAA TCT CGG GAA TCT      96
77 Arg Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser
78      20      25      30
80 CAA TGT      102
81 Gln Cys
85 (2) INFORMATION FOR SEQ ID NO: 2:
87      (i) SEQUENCE CHARACTERISTICS:
88      (A) LENGTH: 34 amino acids
89      (B) TYPE: amino acid
90      (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: protein
94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96 Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg
97 1      5      10      15
99 Arg Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser
100      20      25      30
102 Gln Cys
105 (2) INFORMATION FOR SEQ ID NO: 3:
107      (i) SEQUENCE CHARACTERISTICS:
108      (A) LENGTH: 360 base pairs
109      (B) TYPE: nucleic acid
110      (C) STRANDEDNESS: single
111      (D) TOPOLOGY: linear
113      (ii) MOLECULE TYPE: other nucleic acid
114      (A) DESCRIPTION: /desc = "synthetic DNA"
117      (ix) FEATURE:
118      (A) NAME/KEY: CDS
119      (B) LOCATION: 1..360
122      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
124 ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC      48
125 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
126 1      5      10      15
128 CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT      96
129 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
130      20      25      30
132 GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG      144
133 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
134      35      40      45
136 ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT      192

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137 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
138      50      55      60
140 ATC CCC AAG GCT CGC CGG CCC GAG GGT AGG ACC TGG GCT CAG CCC GGG      240
141 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
142 65      70      75      80
144 TAC CCT TGG CCC CTC TAT GGC AAC GAG GGT ATG GGG TGG GCA GGA TGG      288
145 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
146      85      90      95
148 CTC CTG TCA CCC CGT GGC TCT CGG CCT AGT TGG GGC CCC ACA GAC CCC      336
149 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
150      100      105      110
152 CGG CGT AGG TCG CGT AAT TTG GGT      360
153 Arg Arg Arg Ser Arg Asn Leu Gly
154      115      120
157 (2) INFORMATION FOR SEQ ID NO: 4:
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 120 amino acids
161 (B) TYPE: amino acid
162 (D) TOPOLOGY: linear
164 (ii) MOLECULE TYPE: protein
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
168 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
169 1      5      10      15
171 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
172      20      25      30
174 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
175      35      40      45
177 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
178 50      55      60
180 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
181 65      70      75      80
183 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
184      85      90      95
186 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
187      100      105      110
189 Arg Arg Arg Ser Arg Asn Leu Gly
190      115      120
192 (2) INFORMATION FOR SEQ ID NO: 5:
194 (i) SEQUENCE CHARACTERISTICS:
195 (A) LENGTH: 450 base pairs
196 (B) TYPE: nucleic acid
197 (C) STRANDEDNESS: single
198 (D) TOPOLOGY: linear
200 (ii) MOLECULE TYPE: other nucleic acid
201 (A) DESCRIPTION: /desc = "synthetic DNA"
204 (ix) FEATURE:
205 (A) NAME/KEY: CDS
206 (B) LOCATION: 1..450
209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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211 ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC      48
212 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
213   1           5           10           15
215 CGC CGC CCA CGG GAC GTT AAA TTC CCG GGC GGT GGT CAG ATC GTT GGT      96
216 Arg Arg Pro Arg Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
217           20           25           30
219 GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG      144
220 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
221           35           40           45
223 ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT      192
224 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
225   50           55           60
227 ATC CCC AAG GCT CGC CGG CCC GAG GGT AGG ACC TGG GCT CAG CCC GGG      240
228 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
229 65           70           75           80
231 TAC CCT TGG CCC CTC TAT GGC AAC GAG GGT ATG GGG TGG GCA GGA TGG      288
232 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
233           85           90           95
235 CTC CTG TCA CCC CGT GGC TCC CGG CCT AGT TGG GGC CCC ACG GAC CCC      336
236 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
237   100           105           110
239 CGG CGT AGG TCA CGC AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC      384
240 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
241   115           120           125
243 GGC TTC GCC GAC CTC ATG GGG TAC ATT CCG CTT GTC GGC GCC CCC CTA      432
244 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
245   130           135           140
247 GGG GGC GCT GCC AGG GCC      450
248 Gly Gly Ala Ala Arg Ala
249 145           150
252 (2) INFORMATION FOR SEQ ID NO: 6:
254   (i) SEQUENCE CHARACTERISTICS:
255       (A) LENGTH: 150 amino acids
256       (B) TYPE: amino acid
257       (D) TOPOLOGY: linear
259   (ii) MOLECULE TYPE: protein
261   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
263 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
264   1           5           10           15
266 Arg Arg Pro Arg Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
267           20           25           30
269 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
270           35           40           45
272 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
273   50           55           60
275 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
276 65           70           75           80
278 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
279           85           90           95

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281 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
282      100      105      110
284 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
285      115      120      125
287 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
288      130      135      140
290 Gly Gly Ala Ala Arg Ala
291 145      150
293 (2) INFORMATION FOR SEQ ID NO: 7:
295     (i) SEQUENCE CHARACTERISTICS:
296         (A) LENGTH: 483 base pairs
297         (B) TYPE: nucleic acid
298         (C) STRANDEDNESS: single
299         (D) TOPOLOGY: linear
301     (ii) MOLECULE TYPE: other nucleic acid
302         (A) DESCRIPTION: /desc = "synthetic DNA"
305     (ix) FEATURE:
306         (A) NAME/KEY: CDS
307         (B) LOCATION: 1..483
310     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
312 ATG GCT AGC GAA TTC ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC      48
313 Met Ala Ser Glu Phe Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr
314  1      5      10      15
316 AAA CGT AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC GGT      96
317 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
318      20      25      30
320 GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG      144
321 Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
322      35      40      45
324 TTG GGT GTG CGC GCG ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT      192
325 Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg
326      50      55      60
328 GGA AGG CGA CAA CCT ATC CCC AAG GCT CGC CGG CCC GAG GGT AGG ACC      240
329 Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr
330      65      70      75      80
332 TGG GCT CAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGT ATG      288
333 Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met
334      85      90      95
336 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG CCT AGT TGG      336
337 Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp
338      100      105      110
340 GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT AAT TTG GGT GGA TCC AGA      384
341 Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Gly Ser Arg
342      115      120      125
344 CGA CGA GGC AGG TCC CCT AGA AGA AGA ACT CCC TCG CCT CGC AGA CGA      432
345 Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg
346      130      135      140
348 AGG TCT AAA TCG CCG CGT CGC AGA AGA TCT CAA TCT CGG GAA TCT CAA      480
349 Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\04232002\I306780.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]